

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Maertens, Geert
Bosman, Fons
De Martynoff, Guy
Buyse, Marie-Ange
- (ii) TITLE OF INVENTION: Purified hepatitis C virus envelope
proteins for diagnostic and therapeutic use.
- (iii) NUMBER OF SEQUENCES: 122
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: NIXON & VANDERHYE
 - (B) STREET: 1100 North Glebe Road, 8th Floor
 - (C) CITY: Arlington, VA 22201
 - (E) COUNTRY: USA
 - (F) ZIP: 22201
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Unassigned
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Sadoff, B. J.
 - (B) REGISTRATION NUMBER: 36663
 - (C) REFERENCE/DOCKET NUMBER: 2551-61
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 816-4000
 - (B) TELEFAX: (703) 816-4100

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCATGCAAG CTTAATTAAT T

21

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT
TAACTGCA

60

68

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..639

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Ala Leu Leu Ser Cys
1 5 10 15

48

CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met
20 25 30

96

TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala

144

35	40	45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG			192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu			
50	55	60	
AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT			240
Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala			
65	70	75	80
AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG			288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu			
	85	90	95
CTC GTT GGG GCG GCT GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC			336
Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu			
	100	105	110
TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC			384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg			
	115	120	125
CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC			432
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His			
	130	135	140
ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT			480
Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro			
	145	150	155
ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC			528
Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val			
	165	170	175
GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC			576
Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala			
	180	185	190
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA			624
Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu			
	195	200	205
CTC TTT GCT CTC TAATAG			642
Leu Phe Ala Leu			
210			

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys
1				5					10					15	
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA	672
Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro	
210 215 220	
CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG	720
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala	
225 230 235 240	
GGT CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT	768

795

795

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met 1	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
				5					10					15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35					40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
	50					55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
65					70					75					80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
		115					120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
	130					135					140				
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val
145					150					155					160
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile
				165					170					175	
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr
			180					185					190		
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn
		195					200					205			
Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
	210					215					220				
Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala

(2) INFORMATION FOR SEQ ID NO: 7:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 1..630
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(ix) FEATURE:
      (A) NAME/KEY: mat_peptide
      (B) LOCATION: 1..627
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5				10					15			
ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGT	GCT	GCC	AGA	96
Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20				25					30				
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
		35					40					45				
ACA	GGG	AAT	TTG	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTT	CTC	TTG	GCT	TTA	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55				60						
CTG	TCC	TGT	CTG	ACC	ATT	CCA	GCT	TCC	GCT	TAT	GAG	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
65					70				75					80		
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85				90						95		
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
		100					105					110				

GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACT ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TAATAG	633
Trp	
210	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
 145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
 165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
 180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
 195 200 205

Trp

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..480

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT	48
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG	96
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA	144
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG	192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	

GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC	240
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG	288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC	336
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC	384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	
115 120 125	
CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT	432
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His	
130 135 140	
GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TCC TAATAG	483
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser	
145 150 155 160	

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	
115 120 125	
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His	

130 135 140
 Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..477
- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG TCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT	48
Met Ser Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG	96
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA	144
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG	192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	
GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC	240
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG	288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC	336
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC	384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	

115	120	125	
CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT			432
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His			
130	135	140	
GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG			480
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp			
145	150	155	

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Ser	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys
1				5					10					15	
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val
			20					25					30		
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala
	35					40					45				
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu
	50					55					60				
Gly	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala
65					70					75				80	
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu
			85						90					95	
Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu
			100					105					110		
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
	115						120					125			
Arg	His	Gln	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His
130					135						140				
Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp		
145					150					155					

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG	CTG	GGT	AAG	GCC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Ala	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5					10					15		
GTG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGC	GCT	GCC	AGG	96
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20					25					30			
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
		35				40						45				
ACA	GGG	AAT	TTG	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTA	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55					60					
CTG	TCC	TGT	CTA	ACC	ATT	CCA	GCT	TCC	GCT	TAC	GAG	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
65					70				75					80		
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85				90						95		
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
			100					105					110			
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	
		115					120					125				
CTC	GCG	GCT	AGG	AAC	GCC	AGC	ATC	CCC	ACT	ACA	ACA	ATA	CGA	CGC	CAC	432
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Ile	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	
	130					135						140				
GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	480
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	
145					150					155				160		
GGG	GAT	CTC	TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	ATC	528
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	
				165				170						175		
TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	576
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	

180	185	190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC			624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn			
195	200	205	
TGG TAC TAATAG			640
Trp Tyr			
210			

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Leu	Gly	Lys	Ala	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5				10						15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35					40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
		50				55					60				
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
65					70					75				80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
			115				120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Ile	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
			130				135				140				
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val
145					150					155				160	
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile
				165					170					175	
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr
			180					185					190		
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn
		195					200					205			

Trp Tyr
210

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATGCCCGGTT GCTCTTCTC TATCTT

26

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGTTGGGTA AGGTCATCGA TACCCT

26

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTATTAGGAC CAGTTCATCA TCATATCCCA

30

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTATTACCAG TTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATACGACGCC ACGTCGATTC CCAGCTGTTC ACCATC

36

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GATGGTGAAC AGCTGGGAAT CGACGTGGCG TCGTAT

36

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	

145		150		155		160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT							528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg							
	165			170		175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG							576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val							
	180			185		190	
GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG							624
Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala							
	195			200		205	
GGG GCC CAT TGG GGA GTC CTG GCG GGT CTC GCC TAC TAT TCC ATG GTG							672
Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Ser Met Val							
	210			215		220	
GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC TTT GCT CCC TAATAG							723
Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro							
	225			230		235	240

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5				10						15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25						30	
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
			35					40						45	
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
			50					55						60	
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
			65					70						75	80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85										90	95
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
				100				105						110	
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
				115				120						125	
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
				130				135						140	
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val

145		150		155		160
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg						
	165			170		175
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val						
	180			185		190
Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala						
	195			200		205
Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val						
	210			215		220
Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro						
	225			230		235

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..558

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	

65	70	75	80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG				288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	85	90	95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC				336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	100	105	110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG				384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	115	120	125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC				432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	130	135	140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG				480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	145	150	155	160
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT				528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	165	170	175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG				561
Met Ala Trp Asp Met Met Met Asn Trp	180	185		

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5				10						15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35					40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
	50					55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
65					70					75				80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
 145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
 165 170 175

Met Ala Trp Asp Met Met Met Asn Trp
 180 185

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 606 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..603

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	
145 150 155 160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT	528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	
165 170 175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG	576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val	
180 185 190	
GTA TCG CAG CTG CTC CGG ATC CTC TAATAG	606
Val Ser Gln Leu Leu Arg Ile Leu	
195 200	

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
 100 105 110
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140
 Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
 145 150 155 160
 Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
 165 170 175
 Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
 180 185 190
 Val Ser Gln Leu Leu Arg Ile Leu
 195 200

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192

Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu		
	50					55					60						
CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	240	
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val		
	65				70					75					80		
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val		
				85					90					95			
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys		
			100					105					110				
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384	
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr		
		115					120					125					
CTC	GCA	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	ACA	ATA	CGA	CGC	CAC	432	
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His		
	130					135						140					
GTC	GAT	TCC	CAG	CTG	TTC	ACC	ATC	TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	480	
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val		
	145				150					155					160		
CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	528	
Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg		
			165						170					175			
ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG	576	
Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val		
			180					185					190				
GTA	TCG	CAG	CTG	CTC	CGG	ATC	GTG	ATC	GAG	GGC	AGA	CAC	CAT	CAC	CAC	624	
Val	Ser	Gln	Leu	Leu	Arg	Ile	Val	Ile	Glu	Gly	Arg	His	His	His	His		
		195				200						205					
CAT	CAC	TAATAG														636	
His	His																
	210																

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu		
1				5				10					15				
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg		
		20					25					30					
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala		

35	40	45
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu		
50	55	60
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val		
65	70	75 80
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val		
	85	90 95
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys		
	100	105 110
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr		
	115	120 125
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His		
	130	135 140
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val		
	145	150 155 160
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg		
	165	170 175
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val		
	180	185 190
Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His His		
	195	200 205
His His		
210		

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..627

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGA TTC GCC GAT CTC ATG

Met	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	
1				5					10					15		
GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCT	CCC	GTA	GGA	GGC	GTC	GCA	AGA	GCC	96
Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	
			20					25					30			
CTT	GCG	CAT	GGC	GTG	AGG	GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTC	GCA	ACA	144
Leu	Ala	His	Gly	Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	
		35					40					45				
GGG	AAT	TTG	CCC	GGT	TGC	TCC	TTT	TCT	ATT	TTC	CTT	CTC	GCT	CTG	TTC	192
Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe	
	50					55					60					
TCT	TGC	TTA	ATT	CAT	CCA	GCA	GCT	AGT	CTA	GAG	TGG	CGG	AAT	ACG	TCT	240
Ser	Cys	Leu	Ile	His	Pro	Ala	Ala	Ser	Leu	Glu	Trp	Arg	Asn	Thr	Ser	
	65				70					75					80	
GGC	CTC	TAT	GTC	CTT	ACC	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAC	288
Gly	Leu	Tyr	Val	Leu	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	
			85						90					95		
GAG	GCC	GAT	GAC	GTT	ATT	CTG	CAC	ACA	CCC	GGC	TGC	ATA	CCT	TGT	GTC	336
Glu	Ala	Asp	Gly	Val	Ile	Leu	His	Thr	Pro	Gly	Cys	Ile	Pro	Cys	Val	
			100					105					110			
CAG	GAC	GGC	AAT	ACA	TCC	ACG	TGC	TGG	ACC	CCA	GTG	ACA	CCT	ACA	GTG	384
Gln	Asp	Gly	Asn	Thr	Ser	Thr	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	
		115					120					125				
GCA	GTC	AAG	TAC	GTC	GGA	GCA	ACC	ACC	GCT	TCG	ATA	CGC	AGT	CAT	GTG	432
Ala	Val	Lys	Tyr	Val	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	
		130				135						140				
GAC	CTA	TTA	GTG	GGC	GCG	GCC	ACG	ATG	TGC	TCT	GCG	CTC	TAC	GTG	GGT	480
Asp	Leu	Leu	Val	Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Leu	Tyr	Val	Gly	
	145				150				155					160		
GAC	ATG	TGT	GGG	GCT	GTC	TTC	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	528
Asp	Met	Cys	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	
			165					170						175		
CCT	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	TAC	CCA	576
Pro	Arg	Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	
			180					185					190			
GGC	CAT	CTT	TCA	GGA	CAT	CGA	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	624
Gly	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
		195					200						205			
TAATAG																634

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
 1           5           10           15
Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala
           20           25           30
Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr
           35           40           45
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
           50           55           60
Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser
           65           70           75           80
Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr
           85           90           95
Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val
           100          105          110
Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val
           115          120          125
Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val
           130          135          140
Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly
           145          150          155          160
Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg
           165          170          175
Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro
           180          185          190
Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
           195          200          205

```

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..627

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC GCC GAT CTC ATG	48
Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met	
1 5 10 15	
GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT GGG GGC GTC GCA AGG GCT	96
Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala	
20 25 30	
CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA	144
Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr	
35 40 45	
GGG AAT TTA CCC GGT TGC TCT TTC TCT ATC TTT ATT CTT GCT CTT CTC	192
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu	
50 55 60	
TCG TGT CTG ACC GTT CCG GCC TCT GCA GTT CCC TAC CGA AAT GCC TCT	240
Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser	
65 70 75 80	
GGG ATT TAT CAT GTT ACC AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT	288
Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr	
85 90 95	
GAG GCA GAT AAC CTG ATC CTA CAC GCA CCT GGT TGC GTG CCT TGT GTC	336
Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val	
100 105 110	
ATG ACA GGT AAT GTG AGT AGA TGC TGG GTC CAA ATT ACC CCT ACA CTG	384
Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu	
115 120 125	
TCA GCC CCG AGC CTC GGA GCA GTC ACG GCT CCT CTT CGG AGA GCC GTT	432
Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val	
130 135 140	
GAC TAC CTA GCG GGA GGG GCT GCC CTC TGC TCC GCG TTA TAC GTA GGA	480
Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly	
145 150 155 160	
GAC GCG TGT GGG GCA CTA TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG	528
Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg	
165 170 175	
CCT CGC CAG CAC GCT ACG GTG CAG AAC TGC AAC TGT TCC ATT TAC AGT	576
Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser	
180 185 190	
GGC CAT GTT ACC GGC CAC CGG ATG GCA TGG GAT ATG ATG ATG AAC TGG	624
Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp	
195 200 205	

TAATAG

630

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
 1           5           10           15
Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala
 20           25           30
Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr
 35           40           45
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 50           55           60
Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser
 65           70           75           80
Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr
 85           90           95
Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val
100           105           110
Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu
115           120           125
Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val
130           135           140
Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly
145           150           155           160
Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg
165           170           175
Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser
180           185           190
Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
195           200           205

```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
 TGGGATATGA TGATGAACTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
 CTATTATGGT GGTAAAGCCAC AGAGCAGGAG

30

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1473

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..1470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
 TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG

48

Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	
1					5				10					15		
CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	GTG	GCG	GGG	GCC	96
Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	
			20					25					30			
CAT	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	144
His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	
		35					40					45				
TGG	GCT	AAG	GTT	TTG	GTT	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTC	GAC	GGG	192
Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	
	50					55					60					
CAT	ACC	CGC	GTG	TCA	GGA	GGG	GCA	GCA	GCC	TCC	GAT	ACC	AGG	GGC	CTT	240
His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	
	65				70					75					80	
GTG	TCC	CTC	TTT	AGC	CCC	GGG	TCG	GCT	CAG	AAA	ATC	CAG	CTC	GTA	AAC	288
Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	
				85					90					95		
ACC	AAC	GGC	AGT	TGG	CAC	ATC	AAC	AGG	ACT	GCC	CTG	AAC	TGC	AAC	GAC	336
Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	
			100					105					110			
TCC	CTC	CAA	ACA	GGG	TTC	TTT	GCC	GCA	CTA	TTC	TAC	AAA	CAC	AAA	TTC	384
Ser	Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	
			115				120					125				
AAC	TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	TGT	CGC	TCC	ATC	GAC	432
Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg	Ser	Ile	Asp	
	130					135					140					
AAG	TTC	GCT	CAG	GGG	TGG	GGT	CCC	CTC	ACT	TAC	ACT	GAG	CCT	AAC	AGC	480
Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	Thr	Glu	Pro	Asn	Ser	
	145				150					155					160	
TCG	GAC	CAG	AGG	CCC	TAC	TGC	TGG	CAC	TAC	GCG	CCT	CGA	CCG	TGT	GGT	528
Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly	
				165					170					175		
ATT	GTA	CCC	GCG	TCT	CAG	GTG	TGC	GGT	CCA	GTG	TAT	TGC	TTC	ACC	CCG	576
Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	Tyr	Cys	Phe	Thr	Pro	
			180					185					190			
AGC	CCT	GTT	GTG	GTG	GGG	ACG	ACC	GAT	CGG	TTT	GGT	GTC	CCC	ACG	TAT	624
Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	Gly	Val	Pro	Thr	Tyr	
			195					200				205				
AAC	TGG	GGG	GCG	AAC	GAC	TCG	GAT	GTG	CTG	ATT	CTC	AAC	AAC	ACG	CGG	672
Asn	Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	Leu	Asn	Asn	Thr	Arg	
	210						215					220				
CCG	CCG	CGA	GGC	AAC	TGG	TTC	GGC	TGT	ACA	TGG	ATG	AAT	GGC	ACT	GGG	720
Pro	Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	Gly	Thr	Gly	
	225				230					235					240	
TTC	ACC	AAG	ACG	TGT	GGG	GGC	CCC	CCG	TGC	AAC	ATC	GGG	GGG	GCC	GGC	768
Phe	Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	Ile	Gly	Gly	Ala	Gly	
				245					250					255		

AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG	816
Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu	
260 265 270	
GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT	864
Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys	
275 280 285	
ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC	912
Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn	
290 295 300	
TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG	960
Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg	
305 310 315 320	
TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG	1008
Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu	
325 330 335	
GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG	1056
Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu	
340 345 350	
TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC	1104
Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr	
355 360 365	
GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC	1152
Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr	
370 375 380	
GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC	1200
Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val	
385 390 395 400	
CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA	1248
Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu	
405 410 415	
TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG	1296
Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu	
420 425 430	
GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC	1344
Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser	
435 440 445	
TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC	1392
Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val	
450 455 460	
CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT	1440
Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu	
465 470 475 480	
CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA	1476
Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala	
485 490	

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser
 1             5             10             15
Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala
      20             25             30
His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn
      35             40             45
Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly
      50             55             60
His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu
      65             70             75             80
Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn
      85             90             95
Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp
      100            105            110
Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe
      115            120            125
Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp
      130            135            140
Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser
      145            150            155            160
Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly
      165            170            175
Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro
      180            185            190
Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr
      195            200            205
Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg
      210            215            220
Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly
      225            230            235            240
Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly
      245            250            255
Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu
      260            265            270
Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys

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275	280	285
Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn 290 295 300		
Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg 305 310 315 320		
Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu 325 330 335		
Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu 340 345 350		
Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr 355 360 365		
Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr 370 375 380		
Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val 385 390 395 400		
Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu 405 410 415		
Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu 420 425 430		
Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser 435 440 445		
Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val 450 455 460		
Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu 465 470 475 480		
Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala 485 490		

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1018

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide

(B) LOCATION: 2..1015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA	46
Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly	
1 5 10 15	
GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG	94
Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys	
20 25 30	
GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC	142
Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg	
35 40 45	
GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC	190
Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu	
50 55 60	
TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC	238
Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly	
65 70 75	
AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA	286
Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln	
80 85 90 95	
ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT	334
Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser	
100 105 110	
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT	382
Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala	
115 120 125	
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG	430
Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln	
130 135 140	
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC	478
Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro	
145 150 155	
GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT	526
Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val	
160 165 170 175	
GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG	574
Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly	
180 185 190	
GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA	622
Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg	
195 200 205	
GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG	670
Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys	
210 215 220	
ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC	718
Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr	

225	230	235	
TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC			766
Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr			
240	245	250	255
GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT			814
Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His			
	260	265	270
TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC			862
Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile			
	275	280	285
TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC			910
Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala			
	290	295	300
GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT			958
Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp			
	305	310	315
AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG TGG CAG AGT			1006
Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser			
	320	325	330
GGC AGA GCT TAATTA			1021
Gly Arg Ala			

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val
1				5					10					15	
Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
			20					25					30		
Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val
			35				40					45			
Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe
			50			55					60				
Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser
			65		70				75					80	
Trp	His	Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr
				85				90						95	
Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly
			100					105					110		

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln
 115 120 125
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg
 130 135 140
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala
 145 150 155 160
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val
 165 170 175
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala
 180 185 190
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly
 195 200 205
 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr
 210 215 220
 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu
 225 230 235 240
 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala
 245 250 255
 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr
 260 265 270
 Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe
 275 280 285
 Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala
 290 295 300
 Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg
 305 310 315 320
 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly
 325 330 335
 Arg Ala

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1034 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..1032

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 2..1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA	46
Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly	
1 5 10 15	
GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG	94
Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys	
20 25 30	
GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC	142
Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg	
35 40 45	
GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC	190
Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu	
50 55 60	
TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC	238
Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly	
65 70 75	
AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA	286
Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln	
80 85 90 95	
ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT	334
Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser	
100 105 110	
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT	382
Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala	
115 120 125	
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG	430
Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln	
130 135 140	
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC	478
Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro	
145 150 155	
GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT	526
Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val	
160 165 170 175	
GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG	574
Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly	
180 185 190	
GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA	622
Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg	
195 200 205	

GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys 210 215 220	670
ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr 225 230 235	718
TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr 240 245 250 255	766
GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His 260 265 270	814
TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile 275 280 285	862
TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala 290 295 300	910
GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp 305 310 315	958
AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly 320 325 330 335	1006
CAG ACA CCA TCA CCA CCA TCA CTA AT AG Gln Thr Pro Ser Pro Pro Ser Leu 340	1034

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 343 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val 1 5 10 15
Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val 20 25 30
Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val 35 40 45
Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe 50 55 60
Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser 65 70 75 80

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Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr
      85                      90                      95

Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly
      100                    105                    110

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln
      115                    120                    125

Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg
      130                    135                    140

Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala
145                      150                      155                      160
Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val
      165                    170                    175

Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala
      180                    185                    190

Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly
      195                    200                    205

Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr
      210                    215                    220

Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu
225                      230                      235                      240

Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala
      245                    250                    255

Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr
      260                    265                    270

Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe
      275                    280                    285

Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala
      290                    295                    300

Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg
305                      310                      315                      320

Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly Gln
      325                    330                    335

Thr Pro Ser Pro Pro Ser Leu
      340

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(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..942

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC	48
Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala	
1 5 10 15	
GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT	96
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp	
20 25 30	
ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC	144
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile	
35 40 45	
CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG	192
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu	
50 55 60	
AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC	240
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr	
65 70 75 80	
AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT	288
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys	
85 90 95	
CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT	336
Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr	
100 105 110	
GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT	384
Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro	
115 120 125	
CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT	432
Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr	
130 135 140	
TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT	480
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly	
145 150 155 160	
GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC	528
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu	
165 170 175	
AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG	576
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met	
180 185 190	

AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile 195 200 205	624
GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg 210 215 220	672
AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu 225 230 235 240	720
ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro 245 250 255	768
TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly 260 265 270	816
GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg 275 280 285	864
TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu 290 295 300	912
TCT ACA ACA GAG TGG CAG AGC TTA ATT AAT TAG Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn 305 310	945

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala 1 5 10 15
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp 20 25 30
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile 35 40 45
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu 50 55 60
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr 65 70 75 80
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys 85 90 95

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Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr
      100                      105                      110
Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro
      115                      120                      125
Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr
      130                      135                      140
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly
      145                      150                      155                      160
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu
      165                      170                      175
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met
      180                      185                      190
Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile
      195                      200                      205
Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg
      210                      215                      220
Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu
      225                      230                      235                      240
Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro
      245                      250                      255
Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly
      260                      265                      270
Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg
      275                      280                      285
Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu
      290                      295                      300
Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn
      305                      310

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(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 961 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..958

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide

(B) LOCATION: 1..955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC	48
Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala	
1 5 10 15	
GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT	96
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp	
20 25 30	
ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC	144
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile	
35 40 45	
CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG	192
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu	
50 55 60	
AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC	240
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr	
65 70 75 80	
AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT	288
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys	
85 90 95	
CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT	336
Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr	
100 105 110	
GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT	384
Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro	
115 120 125	
CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT	432
Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr	
130 135 140	
TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT	480
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly	
145 150 155 160	
GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC	528
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu	
165 170 175	
AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG	576
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met	
180 185 190	
AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC	624
Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile	
195 200 205	
GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG	672
Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg	
210 215 220	
AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG	720

Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala
1				5				10						15	
Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp
			20					25					30		
Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile
		35					40					45			
Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	Leu
	50					55					60				
Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr
65					70					75					80
Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys
				85					90					95	
Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	Thr
			100					105					110		
Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	Pro
		115					120					125			
Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	Tyr

130	135	140
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly		
145	150	155 160
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu		
	165	170 175
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met		
	180	185 190
Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile		
	195	200 205
Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg		
	210	215 220
Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu		
	225	230 235 240
Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro		
	245	250 255
Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly		
	260	265 270
Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg		
	275	280 285
Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu		
	290	295 300
Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu		
305	310	315

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1392

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT

Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	
1				5					10					15		
TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	GTT	GTG	ATG	CTA	CTC	TTT	96
Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	
			20					25					30			
GCC	GGC	GTC	GAC	GGG	CAT	ACC	CGC	GTG	TCA	GGA	GGG	GCA	GCA	GCC	TCC	144
Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	
		35					40					45				
GAT	ACC	AGG	GGC	CTT	GTG	TCC	CTC	TTT	AGC	CCC	GGG	TCG	GCT	CAG	AAA	192
Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	
	50					55					60					
ATC	CAG	CTC	GTA	AAC	ACC	AAC	GGC	AGT	TGG	CAC	ATC	AAC	AGG	ACT	GCC	240
Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	
65					70				75						80	
CTG	AAC	TGC	AAC	GAC	TCC	CTC	CAA	ACA	GGG	TTC	TTT	GCC	GCA	CTA	TTC	288
Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	
				85					90					95		
TAC	AAA	CAC	AAA	TTC	AAC	TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	336
Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	
			100					105					110			
TGT	CGC	TCC	ATC	GAC	AAG	TTC	GCT	CAG	GGG	TGG	GGT	CCC	CTC	ACT	TAC	384
Cys	Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	
		115					120					125				
ACT	GAG	CCT	AAC	AGC	TCG	GAC	CAG	AGG	CCC	TAC	TGC	TGG	CAC	TAC	GCG	432
Thr	Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	
	130					135					140					
CCT	CGA	CCG	TGT	GGT	ATT	GTA	CCC	GCG	TCT	CAG	GTG	TGC	GGT	CCA	GTG	480
Pro	Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	
145					150					155					160	
TAT	TGC	TTC	ACC	CCG	AGC	CCT	GTT	GTG	GTG	GGG	ACG	ACC	GAT	CGG	TTT	528
Tyr	Cys	Phe	Thr	Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	
				165				170					175			
GGT	GTC	CCC	ACG	TAT	AAC	TGG	GGG	GCG	AAC	GAC	TCG	GAT	GTG	CTG	ATT	576
Gly	Val	Pro	Thr	Tyr	Asn	Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	
			180					185					190			
CTC	AAC	AAC	ACG	CGG	CCG	CCG	CGA	GGC	AAC	TGG	TTC	GGC	TGT	ACA	TGG	624
Leu	Asn	Asn	Thr	Arg	Pro	Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	
			195				200					205				
ATG	AAT	GGC	ACT	GGG	TTC	ACC	AAG	ACG	TGT	GGG	GGC	CCC	CCG	TGC	AAC	672
Met	Asn	Gly	Thr	Gly	Phe	Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	
	210					215					220					
ATC	GGG	GGG	GCC	GGC	AAC	AAC	ACC	TTG	ACC	TGC	CCC	ACT	GAC	TGT	TTT	720
Ile	Gly	Gly	Ala	Gly	Asn	Asn	Thr	Leu	Thr	Cys	Pro	Thr	Asp	Cys	Phe	
225					230					235					240	
CGG	AAG	CAC	CCC	GAG	GCC	ACC	TAC	GCC	AGA	TGC	GGT	TCT	GGG	CCC	TGG	768
Arg	Lys	His	Pro	Glu	Ala	Thr	Tyr	Ala	Arg	Cys	Gly	Ser	Gly	Pro	Trp	
				245					250					255		

CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC	816
Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr	
260 265 270	
CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG	864
Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly	
275 280 285	
GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG	912
Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu	
290 295 300	
CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG	960
Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu	
305 310 315 320	
CTG TCT ACA ACA GAG TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG	1008
Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu	
325 330 335	
CCG GCC CTA TCC ACC GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC	1056
Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp	
340 345 350	
GTG CAA TAC CTG TAC GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC	1104
Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile	
355 360 365	
AAA TGG GAG TAT GTC CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC	1152
Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Ala Asp Ala Arg	
370 375 380	
ATC TGC GCC TGC TTA TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC	1200
Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala	
385 390 395 400	
GCC TTA GAG AAC CTG GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG	1248
Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala	
405 410 415	
CAT GGC ACT CTT TCC TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC	1296
His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile	
420 425 430	
AAG GGC AGG CTG GTC CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG	1344
Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp	
435 440 445	
CCG CTG CTC CTG CTT CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA	1395
Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala	
450 455 460	

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	1	5	10	15
Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	20	25	30	
Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	35	40	45	
Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	50	55	60	
Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	65	70	75	80
Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	85	90	95	
Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	100	105	110	
Cys	Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	115	120	125	
Thr	Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	130	135	140	
Pro	Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	145	150	155	160
Tyr	Cys	Phe	Thr	Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	165	170	175	
Gly	Val	Pro	Thr	Tyr	Asn	Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	180	185	190	
Leu	Asn	Asn	Thr	Arg	Pro	Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	195	200	205	
Met	Asn	Gly	Thr	Gly	Phe	Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	210	215	220	
Ile	Gly	Gly	Ala	Gly	Asn	Asn	Thr	Leu	Thr	Cys	Pro	Thr	Asp	Cys	Phe	225	230	235	240
Arg	Lys	His	Pro	Glu	Ala	Thr	Tyr	Ala	Arg	Cys	Gly	Ser	Gly	Pro	Trp	245	250	255	
Leu	Thr	Pro	Arg	Cys	Met	Val	His	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	260	265	270	
Pro	Cys	Thr	Val	Asn	Phe	Thr	Ile	Phe	Lys	Val	Arg	Met	Tyr	Val	Gly	275	280	285	
Gly	Val	Glu	His	Arg	Phe	Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	290	295	300	
Arg	Cys	Asp	Leu	Glu	Asp	Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	305	310	315	320

Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu
 325 330 335
 Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp
 340 345 350
 Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile
 355 360 365
 Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg
 370 375 380
 Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala
 385 390 395 400
 Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala
 405 410 415
 His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile
 420 425 430
 Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp
 435 440 445
 Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala
 450 455 460

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2079

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..2076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Thr Leu Gly Gly Ala Ala Arg	
20 25 30	

GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA	672
Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro	
210 215 220	
CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG	720
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala	
225 230 235 240	
GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT	768
Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val	
245 250 255	
GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA	816
Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly	
260 265 270	
GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC	864
Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro	

275	280	285	
GGG TCG GCT CAG AAA ATC Gly Ser Ala Gln Lys Ile 290	CAG CTC GTA AAC ACC AAC Gln Leu Val Asn Thr Asn 295	GGC AGT TGG CAC Gly Ser Trp His 300	912
ATC AAC AGG ACT GCC CTG Ile Asn Arg Thr Ala Leu 305	AAC TGC AAC GAC TCC CTC Asn Cys Asn Asp Ser Leu 310	CAA ACA GGG TTC Gln Thr Gly Phe 315	960
TTT GCC GCA CTA TTC TAC Phe Ala Ala Leu Phe Tyr 325	AAA CAC AAA TTC AAC Lys His Lys Phe Asn 330	TCT GGA TGC CCA Ser Ser Gly Cys Pro 335	1008
GAG CGC TTG GCC AGC TGT Glu Arg Leu Ala Ser Cys 340	CGC TCC ATC GAC AAG TTC Arg Ser Ile Asp Lys Phe 345	GCT CAG GGG TGG Ala Gln Gly Trp 350	1056
GGT CCC CTC ACT TAC ACT Gly Pro Leu Thr Tyr Thr 355	GAG CCT AAC AGC TCG GAC Glu Pro Asn Ser Ser Asp 360	CAG AGG CCC TAC Gln Arg Pro Tyr 365	1104
TGC TGG CAC TAC GCG CCT Cys Trp His Tyr Ala Pro 370	CGA CCG TGT GGT ATT GTA Arg Pro Cys Gly Ile Val 375	CCC GCG TCT CAG Pro Ala Ser Gln 380	1152
GTG TGC GGT CCA GTG TAT Val Cys Gly Pro Val Tyr 385	TGC TTC ACC CCG AGC CCT Cys Phe Thr Pro Ser Pro 390	GTT GTG GTG GGG Val Val Val Gly 395	1200
ACG ACC GAT CGG TTT GGT Thr Thr Asp Arg Phe Gly 405	GTC CCC ACG TAT AAC TGG Val Pro Thr Tyr Asn Trp 410	GGG GCG AAC GAC Gly Ala Asn Asp 415	1248
TCG GAT GTG CTG ATT CTC Ser Asp Val Leu Ile Leu 420	AAC AAC ACG CGG CCG CCG Asn Asn Thr Arg Pro Pro 425	CGA GGC AAC TGG Arg Gly Asn Trp 430	1296
TTC GGC TGT ACA TGG ATG Phe Gly Cys Thr Trp Met 435	AAT GGC ACT GGG TTC ACC Asn Gly Thr Gly Phe Thr 440	AAG ACG TGT GGG Lys Thr Cys Gly 445	1344
GGC CCC CCG TGC AAC ATC Gly Pro Pro Cys Asn Ile 450	GGG GGC GCC GGC AAC AAC Gly Gly Ala Gly Asn Asn 455	ACC TTG ACC TGC Thr Leu Thr Cys 460	1392
CCC ACT GAC TGT TTT CGG Pro Thr Asp Cys Phe Arg 465	AAG CAC CCC GAG GCC ACC Lys His Pro Glu Ala Thr 470	TAC GCC AGA TGC Tyr Ala Arg Cys 475	1440
GGT TCT GGG CCC TGG CTG Gly Ser Gly Pro Trp Leu 485	ACA CCT AGG TGT ATG GTT Thr Pro Arg Cys Met Val 490	CAT TAC CCA TAT His Tyr Pro Tyr 495	1488
AGG CTC TGG CAC TAC CCC Arg Leu Trp His Tyr Pro 500	TGC ACT GTC AAC TTC ACC Cys Thr Val Asn Phe Thr 505	ATC TTC AAG GTT Ile Phe Lys Val 510	1536
AGG ATG TAC GTG GGG GGC Arg Met Tyr Val Gly Gly 515	GTG GAG CAC AGG TTC GAA Val Glu His Arg Phe Glu 520	GCC GCA TGC AAT Ala Ala Cys Asn 525	1584
TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC TGT GAC AGG GAT AGA TCA GAG			1632

Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu	
530 535 540	
CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG TGG CAG ATA CTG CCC TGT	1680
Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys	
545 550 555 560	
TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC GGC CTG ATC CAC CTC CAT	1728
Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His	
565 570 575	
CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC GGT GTA GGG TCG GCG GTT	1776
Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val	
580 585 590	
GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC CTG TTG CTC TTC CTT CTC	1824
Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu	
595 600 605	
CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA TGG ATG ATG CTG CTG ATA	1872
Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile	
610 615 620	
GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG GTG GTC CTC AAT GCG GCG	1920
Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala	
625 630 635 640	
GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC TTC CTT GTG TTC TTC TGT	1968
Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys	
645 650 655	
GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC CCT GGT GCG GCA TAC GCC	2016
Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala	
660 665 670	
TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT CTG CTG GCC TTA CCA CCA	2064
Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro	
675 680 685	
CGA GCT TAT GCC TAGTAA	2082
Arg Ala Tyr Ala	
690	

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	

35					40					45					
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
50						55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
65					70					75					80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
	115						120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
130						135						140			
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val
145					150					155					160
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile
			165					170						175	
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr
			180					185					190		
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn
	195					200						205			
Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
210					215						220				
Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala
225					230					235					240
Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val
			245						250					255	
Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly
		260					265						270		
Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro
	275					280						285			
Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His
290					295						300				
Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe
305				310						315					320
Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro
			325						330					335	
Glu	Arg	Leu	Ala	Ser	Cys	Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp
		340						345					350		
Gly	Pro	Leu	Thr	Tyr	Thr	Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr
	355					360						365			
Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln

370	375	380
Val Cys Gly Pro Val	Tyr Cys Phe Thr Pro	Ser Pro Val Val Val Gly
385	390	395 400
Thr Thr Asp Arg Phe	Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp	
	405 410	415
Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp		
	420 425	430
Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly		
	435 440	445
Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys		
	450 455	460
Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys		
	465 470	475 480
Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr		
	485 490	495
Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val		
	500 505	510
Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn		
	515 520	525
Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu		
	530 535	540
Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys		
	545 550	555 560
Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His		
	565 570	575
Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val		
	580 585	590
Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu		
	595 600	605
Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile		
	610 615	620
Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala		
	625 630	635 640
Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys		
	645 650	655
Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala		
	660 665	670
Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro		
	675 680	685
Arg Ala Tyr Ala		
	690	

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2430

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..2427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT	96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGG AGG CGA CAA CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCT CGC CGA CCC GAG GGT AGG GCC TGG GCT CAG CCC GGG	240
Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly	
65 70 75 80	
TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG GGG TGG GCA GGA TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCA CCC CGC GGC TCT CGG CCT AGT TGG GGC CCT ACA GAC CCC	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	
100 105 110	
CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC	384
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGC TTC GCC GAC CTC GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA	432
Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu	
130 135 140	
GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC	480

Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	
145					150					155					160	
GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	TTG	CCC	GGT	TGC	TCT	TTC	TCT	ATC	528
Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	
				165				170						175		
TTC	CTC	TTG	GCT	TTG	CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	576
Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	
			180					185					190			
GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	624
Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	
		195					200					205				
AAC	TCA	AGC	ATT	GTG	TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	672
Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	
	210					215					220					
GGG	TGC	GTG	CCC	TGC	GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	720
Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	
225					230					235				240		
GCG	CTC	ACC	CCC	ACG	CTC	GCA	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	768
Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	
				245					250					255		
ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	GCT	TTC	TGT	816
Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	
			260					265					270			
TCC	GCT	ATG	TAC	GTG	GGG	GAC	CTC	TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	864
Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	
		275					280					285				
CAG	CTG	TTC	ACC	ATC	TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	912
Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	
	290					295					300					
AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	ATG	GCT	TGG	960
Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	
305					310					315				320		
GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG	GTA	TCG	CAG	1008
Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	
				325					330					335		
CTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	GTG	GCG	GGG	GCC	CAT	1056
Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	
			340					345					350			
TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	1104
Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	
	355						360					365				
GCT	AAG	GTT	TTG	GTT	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTC	GAC	GGG	CAT	1152
Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	
	370					375					380					
ACC	CGC	GTG	TCA	GGA	GGG	GCA	GCA	GCC	TCC	GAT	ACC	AGG	GGC	CTT	GTG	1200
Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val	
385					390					395				400		

TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr 405 410 415	1248
AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser 420 425 430	1296
CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn 435 440 445	1344
TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys 450 455 460	1392
TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser 465 470 475 480	1440
GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile 485 490 495	1488
GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser 500 505 510	1536
CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn 515 520 525	1584
TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro 530 535 540	1632
CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe 545 550 555 560	1680
ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn 565 570 575	1728
AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala 580 585 590	1776
ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met 595 600 605	1824
GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe 610 615 620	1872
ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe 625 630 635 640	1920
GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC	1968

Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp	
645	650 655
AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG TCT ACA ACA GAG TGG	2016
Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp	
660	665 670
CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC GGC	2064
Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly	
675	680 685
CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC GGT	2112
Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly	
690	695 700
GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC CTG	2160
Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu	
705	710 715 720
TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA TGG	2208
Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp	
725	730 735
ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG GTG	2256
Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val	
740	745 750
GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC TTC	2304
Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe	
755	760 765
CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC CCT	2352
Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro	
770	775 780
GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT CTG	2400
Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu	
785	790 795 800
CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA	2433
Leu Ala Leu Pro Pro Arg Ala Tyr Ala	
805	810

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 809 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
			20					25					30		
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala

35					40					45					
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
50						55					60				
Ile	Pro	Lys	Ala	Arg	Arg	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly
65					70					75					80
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp
				85					90					95	
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
			100					105					110		
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys
			115				120				125				
Gly	Phe	Ala	Asp	Leu	Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu
	130					135					140				
Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp
145					150					155					160
Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile
				165					170					175	
Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr
			180					185					190		
Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser
			195				200						205		
Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro
			210			215					220				
Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val
225					230					235					240
Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr
				245					250					255	
Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys
			260					265					270		
Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser
			275				280					285			
Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys
	290					295					300				
Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp
305					310					315					320
Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln
				325					330					335	
Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His
			340					345					350		
Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp
			355				360						365		
Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His

370	375	380
Thr Arg Val Ser Gly 385	Gly Ala Ala Ala Ser 390	Asp Thr Arg Gly Leu Val 395 400
Ser Leu Phe Ser 405	Pro Gly Ser Ala Gln Lys 410	Ile Gln Leu Val Asn Thr 415
Asn Gly Ser Trp His 420	Ile Asn Arg Thr Ala Leu 425	Asn Cys Asn Asp Ser 430
Leu Gln Thr Gly Phe 435	Phe Ala Ala Leu Phe Tyr 440	Lys His Lys Phe Asn 445
Ser Ser Gly Cys Pro 450	Glu Arg Leu Ala Ser Cys 455	Arg Ser Ile Asp Lys 460
Phe Ala Gln Gly Trp 465	Gly Pro Leu Thr Tyr 470	Thr Glu Pro Asn Ser Ser 475 480
Asp Gln Arg Pro Tyr 485	Cys Trp His Tyr Ala Pro 490	Arg Pro Cys Gly Ile 495
Val Pro Ala Ser Gln 500	Val Cys Gly Pro Val Tyr 505	Cys Phe Thr Pro Ser 510
Pro Val Val Val Gly 515	Thr Thr Asp Arg Phe Gly 520	Val Pro Thr Tyr Asn 525
Trp Gly Ala Asn Asp 530	Ser Asp Val Leu Ile Leu 535	Asn Asn Thr Arg Pro 540
Pro Arg Gly Asn Trp 545	Phe Gly Cys Thr Trp Met 550	Asn Gly Thr Gly Phe 555 560
Thr Lys Thr Cys Gly 565	Gly Pro Pro Cys Asn 570	Ile Gly Gly Ala Gly Asn 575
Asn Thr Leu Thr Cys 580	Pro Thr Asp Cys Phe Arg 585	Lys His Pro Glu Ala 590
Thr Tyr Ala Arg Cys 595	Gly Ser Gly Pro Trp Leu 600	Thr Pro Arg Cys Met 605
Val His Tyr Pro Tyr 610	Arg Leu Trp His Tyr Pro 615	Cys Thr Val Asn Phe 620
Thr Ile Phe Lys Val Arg 625	Met Tyr Val Gly Gly Val 630	Glu His Arg Phe 635 640
Glu Ala Ala Cys Asn Trp 645	Thr Arg Gly Glu Arg Cys 650	Asp Leu Glu Asp 655
Arg Asp Arg Ser Glu 660	Leu Ser Pro Leu Leu Ser 665	Thr Thr Glu Trp 670
Gln Ile Leu Pro Cys Ser 675	Phe Thr Thr Leu Pro Ala 680	Leu Ser Thr Gly 685
Leu Ile His Leu His Gln 690	Asn Ile Val Asp Val Gln 695	Tyr Leu Tyr Gly 700

Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu
 705 710 715 720

Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp
 725 730 735

Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val
 740 745 750

Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe
 755 760 765

Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro
 770 775 780

Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu
 785 790 795 800

Leu Ala Leu Pro Pro Arg Ala Tyr Ala
 805

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys
 1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 1 5 10 15

Ser Pro Thr Thr Ala Leu
 20

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
 1 5 10 15

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr
 20 25 30

Pro Gly Cys Gly Lys
 35

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr
 1 5 10 15

Gln Leu Arg Arg His Ile Asp Leu Leu
 20 25

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Gly	Gly	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asp	Ala	Ser	Val	Pro	Thr	Thr
1				5				10						15	
Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu							
				20				25							

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Gln	Val	Arg	Asn
1				5				10						15	
Ser	Thr	Gly	Leu												
			20												

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	Cys	Pro
1				5				10						15	
Asn	Ser	Ser	Ile												
			20												

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile
 1 5 10 15
 Leu His Thr Pro
 20

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr
 1 5 10 15
 Pro Gly Cys Val
 20

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

His Asp Ala Ile Leu His Thr Pro Gly Val Pro Cys Val Arg Glu Gly
 1 5 10 15
 Asn Val Ser

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro
 1 5 10 15

Thr Val Ala Thr
 20

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr
 1 5 10 15

Gln Leu Arg Arg
 20

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser
 1 5 10 15

Ala Thr Leu Cys
 20

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Leu Val Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu
1 5 10 15

Cys Gly Ser Val
20

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Gly Cys
1 5 10 15

Asn Cys Ser Ile
20

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His
1 5 10 15

Arg Met Ala Trp
20

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro
 1 5 10 15
 Thr Ala Ala Leu
 20

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile
 1 5 10 15
 Pro Gln Ala Ile
 20

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His
 1 5 10 15
 Trp Gly Val Leu
 20

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met
1				5					10					15	
Val Gly Asn Met															
20															

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala	Glu	Thr	Ile	Val	Ser
1				5					10					15	
Gly Gly Gln Ala															
20															

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser	Gly	Leu	Val	Ser	Leu	Phe	Thr	Pro	Gly	Ala	Lys	Gln	Asn	Ile	Gln
1				5					10					15	
Leu Ile Asn Thr															
20															

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Gln	Asn	Ile	Gln	Leu	Ile	Asn	Thr	Asn	Gly	Gln	Trp	His	Ile	Asn	Ser
1				5					10					15	
Thr Ala Leu Asn															
20															

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Leu	Asn	Cys	Asn	Glu	Ser	Leu	Asn	Thr	Gly	Trp	Trp	Leu	Ala	Gly	Leu
1				5					10					15	
Ile Tyr Gln His Lys															
20															

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala	Gly	Leu	Ile	Tyr	Gln	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu
1				5					10					15	
Arg Leu Ala Ser															
20															

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp

1	5	10	15
Gln Gly Trp Gly			
20			

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Thr	Asp	Phe	Asp	Gln	Gly	Trp	Gly	Pro	Ile	Ser	Tyr	Ala	Asn	Gly	Ser
1				5				10						15	

Gly	Pro	Asp	Gln
			20

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala	Asn	Gly	Ser	Gly	Pro	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Pro
1				5				10						15	

Pro	Lys	Pro	Cys
			20

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Trp	His	Tyr	Pro	Pro	Lys	Pro	Cys	Gly	Ile	Val	Pro	Ala	Lys	Ser	Val
1					5				10					15	

Cys	Gly	Pro	Val
-----	-----	-----	-----

20

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ala	Lys	Ser	Val	Cys	Gly	Pro	Val	Tyr	Cys	Phe	Thr	Pro	Ser	Pro	Val
1				5				10						15	
Val Val Gly Thr															
20															

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Ser	Gly	Ala	Pro	Thr
1				5					10					15	
Tyr Ser Trp Gly															
20															

(2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Gly	Ala	Pro	Thr	Tyr	Ser	Trp	Gly	Glu	Asn	Asp	Thr	Asp	Val	Phe	Val
1				5				10						15	
Leu Asn Asn Thr															
20															

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	Ser	Thr	Gly	Phe	Thr	Lys
1				5				10						15	
Val Cys Gly Ala															
20															

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Gly	Phe	Thr	Lys	Val	Cys	Gly	Ala	Pro	Pro	Val	Cys	Ile	Gly	Gly	Ala
1				5				10						15	
Gly Asn Asn Thr															
20															

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Ile	Gly	Gly	Ala	Gly	Asn	Asn	Thr	Leu	His	Cys	Pro	Thr	Asp	Cys	Arg
1				5				10						15	
Lys His Pro															

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly
 1 5 10 15

Ser Gly Pro Trp
 20

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp
 1 5 10 15

Tyr Pro Tyr Arg
 20

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile
 1 5 10 15

Asn Tyr Thr Ile
 20

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Pro	Cys	Thr	Ile	Asn	Tyr	Thr	Ile	Phe	Lys	Ile	Arg	Met	Tyr	Val	Gly
1				5					10					15	
Gly Val Glu His															
20															

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Met	Tyr	Val	Gly	Gly	Val	Glu	His	Arg	Leu	Glu	Ala	Ala	Cys	Asn	Trp
1				5					10					15	
Thr Pro Gly Glu															
20															

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ala	Cys	Asn	Trp	Thr	Pro	Gly	Glu	Arg	Cys	Asp	Leu	Glu	Asp	Arg	Asp
1				5					10					15	
Arg Ser Glu Leu															
20															

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr Thr
1 5 10 15
Gln Trp Gln Val
20

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr Gln Val Arg Asn Ser Thr Gly Leu
1 5

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ACGTCCGTAC GTTCGAATTA ATTAATCGA

29

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CCTCCGGACG TGCCTAGCT CCCGTCTGTG GTAGTGGTGG TAGTGATTAT CAATTAATTG

60

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GTTTAACCAC TGCATGATG

19

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GTCCCATCGA GTGCGGCTAC

20

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CGTGACATGG TACATTCCGG ACACTTGGCG CACTTCATAA GCGGA

45

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TGCCTCATAC ACAATGGAGC TCTGGGACGA GTCGTTCTGTG AC

42

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TACCCAGCAG CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC

42

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TGTCGTGGTG GGGACGGAGG CCTGCCTAGC TGCAGCGTG GG

42

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CGTTATGTGG CCCGGGTAGA TTGAGCACTG GCAGTCCTGC ACCGTCTC

48

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CAGGGCCGTT CTAGGCCTCC ACTGCATCAT CATATCCCAA GC

42

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CCGGAATGTA CCATGTCACG AACGAC

26

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GCTCCATTGT GATGAGGCA GCGG

24

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GAGCTCCCGC TGCTGGGTAG CGC

23

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CCTCCGTCCC CACCACGACA ATACG

25

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CTACCCGGGC CACATAACGG GTCACCG

27

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGAGGCCTAC AACGGCCCTG GTGG

24

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTCTATCGAT TAAATAGAAT TC

22

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GCCATACGCT CACAGCCGAT CCC

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
 1 5 10 15
 Ser Asn Ser Ser
 20

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp
 1 5 10 15
 Met Ile Met His Thr
 20

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val
 1 5 10 15

Arg Glu Asn Asn Ser
20

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu
1 5 10 15

Thr Pro Thr Leu Ala
20

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro
1 5 10 15

Thr Thr Thr Ile Arg
20

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
1					5				10					15
Gly Ala Ala Ala Phe														
20														

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly
1					5				10					15
Asp Leu Cys Gly Ser														
20														

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu
1					5				10					15
Phe Thr Ile Ser Pro														
20														

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln
1				5				10					15	
Asp Cys Asn Cys Ser														
20														

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr
1				5				10					15	
Gly His Arg Met Ala														
20														

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
1				5				10					15	
Ser Pro Thr Thr Ala														
20														